**Description of Additional Supplementary Files**

**File name: Supplementary Movie 1**
Description: Time lapse movies of a wild-type embryo in which endogenous Her7 can be visualized by tagging with three copies of the Achilles, fast-maturing YFP variant at 1 frame/min.

**File name: Supplementary Movie 2**
Description: Time lapse movies of a *ripply1; ripply2* double-mutant embryo in which endogenous Her7 can be visualized by tagging with three copies of the Achilles, fast-maturing YFP variant at 1 frame/min.

**File name: Supplementary Movie 3**
Description: The result of mathematical simulation of wild-type embryos showing temporal changes in Her protein (green), dpErk (orange), Tbx6 protein (cyan), *ripply-intron* mRNA (magenta) and Ripply protein (black). The horizontal axis indicates space (μm: anterior on the left) and the vertical axis indicates relative levels of mRNA and proteins.

**File name: Supplementary Movie 4**
Description: The result of mathematical simulation without the positive feedback loop of Tbx6 protein. Spatial patterns of Her protein (green), *ripply-intron* mRNA (magenta), Ripply protein (black), Tbx6 protein (cyan) and dpErk protein (orange) are shown. The horizontal axis indicates space (μm: anterior on the left) and the vertical axis indicates relative levels of mRNA and proteins. The positive feedback loop in the equation for Tbx6 protein levels was replaced with a constant value.

**File name: Supplementary Movie 5**
Description: The result of mathematical simulation of *ripply*-defective embryos showing temporal changes in *her-intron* mRNA (green) and *her-exon* mRNA (magenta), compared with those of dpErk protein (orange) and Tbx6 protein (cyan). (Top) Simulation of wild type with *ripply* transcription. (Bottom) Simulation of *ripply* KO by setting the maximum transcription rate of *ripply* mRNA to zero. The horizontal axis indicates space (μm: anterior on the left) and the vertical axis indicates relative levels of mRNAs and proteins. To show oscillation in the anterior part, we used an array of $N = 63$ cells. The array represents the tissue region 630 μm anterior to the tailbud.

**File name: Supplementary Movie 6**
Description: The result of mathematical simulation of *her*-defective embryos showing temporal changes in *ripply-intron* mRNA (magenta) with those of dpErk (orange) and Tbx6 proteins (cyan). The horizontal axis indicates space (μm: anterior on the left) and the vertical axis indicates relative levels of mRNA and proteins. At $t = 82$ min, dpErk activity was reduced by 10-fold to model the effect of MEK1 inhibitor. To model *her* KO, we multiplied the transcription term of *her* mRNA by zero.

**File name: Supplementary Movie 7**
Description: The result of mathematical simulation of wild-type embryos, similar to Supplementary Movie 3, but with a stepwise retreat of dpErk activity. Spatial patterns of Her protein (green), *ripply-intron* mRNA (magenta), Ripply protein (black), Tbx6 protein (cyan) and dpErk protein (orange) are shown. The horizontal axis indicates space (μm: anterior on the left) and the vertical axis indicates relative levels of mRNA and proteins. The position of the anterior border of dpErk protein shifts at each oscillation cycle.

**File name: Supplementary Software 1**
Description: The C program and Mathematica codes that were used to simulate the mathematical model and visualize results.